PATENT COOPERATION TREATY

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NOTIFICATION CONCERNING SUBMISSION OR TRANSMITTAL OF PRIORITY DOCUMENT

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Date of mailing (day/month/year) 19 November 2003 (19.11.03)	
Applicant's or agent's file reference 12186WO	**IMPORTANT NOTIFICATION**
International application No. PCT/EP03/09968	International filing date (day/month/year) 08 September 2003 (08.09.03)
International publication date (day/month/year) Not yet published	Priority date (day/month/year) 11 September 2002 (11.09.02)
Applicant ESPLORA GMBH et al	

1. The applicant is hereby notified of the date of receipt (except where the letters "NR" appear in the right-hand column) by the International Bureau of the priority document(s) relating to the earlier application(s) indicated below. Unless otherwise indicated by an asterisk appearing next to a date of receipt, or by the letters "NR", in the right-hand column, the priority document concerned was submitted or transmitted to the International Bureau in compliance with Rule 17.1(a) or (b).

2. This updates and replaces any previously issued notification concerning submission or transmittal of priority documents.

3. An **asterisk(*)** appearing next to a date of receipt, in the right-hand column, denotes a priority document submitted or transmitted to the International Bureau but not in compliance with Rule 17.1(a) or (b). In such a case, **the attention of the applicant is directed** to Rule 17.1(c) which provides that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity, upon entry into the national phase, to furnish the priority document within a time limit which is reasonable under the circumstances.

4. The **letters "NR"** appearing in the right-hand column denote a priority document which was not received by the International Bureau or which the applicant did not request the receiving Office to prepare and transmit to the International Bureau, as provided by Rule 17.1(a) or (b), respectively. In such a case, **the attention of the applicant is directed** to Rule 17.1(c) which provides that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity, upon entry into the national phase, to furnish the priority document within a time limit which is reasonable under the circumstances.

Priority date	Priority application No.	Country or regional Office or PCT receiving Office	Date of receipt of priority document
11 Sept 2002 (11.09.02) ✓	102 42 016.5 ✓	DE ✓	14 Nove 2003 (14.11.03)

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SEQUENCE LISTING

<110> FrankGen Biotechnologie AG

<120> Method for identifying BBB-specific proteins and fragments thereof

<130> 12186WO

<140>
<141>

<160> 58

<170> PatentIn Ver. 2.1

<210> 1
<211> 323
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Clone S129 from BMEC from swine brain

<400> 1
ctgcagccga ggacaacact gattcgagcc gtgacctacc ggccgcggga attcgattta 60
tggtgaaaat cgccttcaat acacccgcag cggtgcaaaa agaggaggcg cagcaagacg 120
tggaggccct cgtaagccat acggtccgtg ctcagatcct gactggcaag gaactccaag 180
ttgccactaa ggaaaaagag ggcttctctg ggagatgcat gcttactctc gtaggccttt 240
ccttcatctt ggcaggactt attgttggtg gagcctgcat ttacaagtac ttcatgccca 300
agagtaccat actaccatgg aga 323

<210> 2
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 2
acctccattg ttatgcctcc ta 22

<210> 3
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 3
gttgcctctc actcttgaca ga 22

<210> 4
<211> 1598
<212> DNA
<213> Swine

<220>
<221> CDS
<222> (119)..(910)

<400> 4

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gcggccgcta gcataaagaa ggtgattcta agcctagcgc tatcttctcc tagtccagcc 60

tgcagccgag gacaacactg attcgagccg tgacctaccg gccgcgggaa ttcgattt   118

atg gtg aaa atc gcc ttc aat aca ccc gca gcg gtg caa aaa gag gag   166
Met Val Lys Ile Ala Phe Asn Thr Pro Ala Ala Val Gln Lys Glu Glu
  1               5                  10                  15

gcg cag caa gac gtg gag gcc ctc gta agc cat acg gtc cgt gct cag   214
Ala Gln Gln Asp Val Glu Ala Leu Val Ser His Thr Val Arg Ala Gln
            20                  25                  30

atc ctg act ggc aag gaa ctc caa gtt gcc act aag gaa aaa gag ggc   262
Ile Leu Thr Gly Lys Glu Leu Gln Val Ala Thr Lys Glu Lys Glu Gly
        35                  40                  45

ttc tct ggg aga tgc atg ctt act ctc gta ggc ctt tcc ttc atc ttg   310
Phe Ser Gly Arg Cys Met Leu Thr Leu Val Gly Leu Ser Phe Ile Leu
    50                  55                  60

gca gga ctt att gtt ggt gga gcc tgc att tac aag tac ttc atg ccc   358
Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
65                  70                  75                  80

aag agt acc atc tac cat gga gag atg tgc ttc ttt gat tct gcg gac   406
Lys Ser Thr Ile Tyr His Gly Glu Met Cys Phe Phe Asp Ser Ala Asp
                85                  90                  95

cct gca aat ttc ctc caa gga gga gag ccc tac ttc ctg cct gtg atg   454
Pro Ala Asn Phe Leu Gln Gly Gly Glu Pro Tyr Phe Leu Pro Val Met
            100                 105                 110

gaa gag gct gat att cgt gaa gat gac aac att gca atc att gat gtg   502
Glu Glu Ala Asp Ile Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val
        115                 120                 125

cct gtc ccc agt ttc tct gat agt gac cct gca gca att att cat gac   550
Pro Val Pro Ser Phe Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp
    130                 135                 140

ttt gaa aag ggc atg act gct tac ctg gac ttg ctg ctg ggg aac tgc   598
Phe Glu Lys Gly Met Thr Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys
145                 150                 155                 160

tat ctg atg ccc ctc aat acc tcc att gtt atg cct cct aag tat ctc   646
Tyr Leu Met Pro Leu Asn Thr Ser Ile Val Met Pro Pro Lys Tyr Leu
                165                 170                 175

gtg gag ctc ttt ggc aaa ctg gca cgt ggc aaa tac ctc cct cac gct   694
Val Glu Leu Phe Gly Lys Leu Ala Arg Gly Lys Tyr Leu Pro His Ala
            180                 185                 190

tat gtg gtt cat gaa gac ctg gtt gct gtg gaa gag att cat gat gtt   742
Tyr Val Val His Glu Asp Leu Val Ala Val Glu Glu Ile His Asp Val
        195                 200                 205

agt aac ctt ggc atc ttt att tac caa ctt tgc aac aac cgc aag tct   790
Ser Asn Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser
    210                 215                 220

ttc cgc ctt cgt aga aga gac ctc ttg ctg ggt ttc aac aaa cgt gcc   838
Phe Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala
225                 230                 235                 240

att gat aag tgc tgg aag att aga cac ttc ccc aat gaa ttt att gtt   886
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val
                245                 250                 255
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gag acc aag atc tgt caa gag tga gaggcaacag aaaaagagtg tacttagtaa  940
Glu Thr Lys Ile Cys Gln Glu
            260

taggaagtca aagatttaca atatgacttc aatattaaag tgtgtaggac attcaagata 1000

tttactcatg catttcctct attgcttata cttaaaaaaa agaaagaaaa taaaaactac 1060

taaccattgc aaaaaaaaaa aaaaaaagta ctagtcgacg cgtggccaga aactgaaatg 1120

aaatgatttt tatgtttttc cttttgaatt tatagggttt atgttttntt gaatgcaatg 1180

tgaaggtgtt ggctaacatc ctgacaatga attccatccc ttgtgtatat gtgtgtcttt 1240

aaaagtaaaa tyttcartca tatggtaaaa catgttttaa atttaaaata tttaaaattg 1300

ttttcaacct ttttgtgtag cgcttgtcaa atatcttaac attgtcttgt tttgttttca 1360

ttgtgtgcaa ctttcctgaa tttagaaatt aaatttttgc atttatgtta ggtgttctgt 1420

aatagatatg acttatatgt gaaaaacttt cataaagaag tcattttcac taatrcagtg 1480

actctcactg gtaactgtat tgtgaaatgc acaaaactgt tttagtgctg aatgctataa 1540

ggaatttagg ttgtatgaat tctacaatcc tataataaat tttaccatat tcaaaaaa   1598
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<210> 5
<211> 263
<212> PRT
<213> Swine

<400> 5

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Met Val Lys Ile Ala Phe Asn Thr Pro Ala Ala Val Gln Lys Glu Glu
  1               5                  10                  15
Ala Gln Gln Asp Val Glu Ala Leu Val Ser His Thr Val Arg Ala Gln
            20                  25                  30
Ile Leu Thr Gly Lys Glu Leu Gln Val Ala Thr Lys Glu Lys Glu Gly
        35                  40                  45
Phe Ser Gly Arg Cys Met Leu Thr Leu Val Gly Leu Ser Phe Ile Leu
    50                  55                  60
Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
65                  70                  75                  80
Lys Ser Thr Ile Tyr His Gly Glu Met Cys Phe Phe Asp Ser Ala Asp
                85                  90                  95
Pro Ala Asn Phe Leu Gln Gly Gly Glu Pro Tyr Phe Leu Pro Val Met
            100                 105                 110
Glu Glu Ala Asp Ile Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val
        115                 120                 125
Pro Val Pro Ser Phe Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp
    130                 135                 140
Phe Glu Lys Gly Met Thr Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys
145                 150                 155                 160
Tyr Leu Met Pro Leu Asn Thr Ser Ile Val Met Pro Pro Lys Tyr Leu
                165                 170                 175
Val Glu Leu Phe Gly Lys Leu Ala Arg Gly Lys Tyr Leu Pro His Ala
            180                 185                 190
Tyr Val Val His Glu Asp Leu Val Ala Val Glu Glu Ile His Asp Val
        195                 200                 205
Ser Asn Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser
    210                 215                 220
Phe Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala
225                 230                 235                 240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val
                245                 250                 255
Glu Thr Lys Ile Cys Gln Glu
            260
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<210> 6
<211> 814
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Clone S231
from BMEC from swine brain

<400> 6
acatttcttt aggttcattc tggttaaggg gatgttcgag ggtgggccac caaattgtct 60
gggctgggga taaagcagtt ggcaagcaaa aactatggga tgatgaactt ttcaatwatg 120
atttaatgat cacatgagta tagaaagctg ttttgagtgc tgaaacagac ttacctatca 180
gatatatcca aaagagattc tatgttaaaa agtcagacta tgactggagt gaaccatgta 240
ttcccttgtc ttttactttg tttctgtgac atttatgttt catgtaactt gcattatggt 300
tgggtgggtt gtcctagtac tgtattttgg cttcttcttt aataggattg atatttcata 360
tabtataatt gtgaatattt tgakacraat gtttataact ctaggcatat aaaaacagat 420
tctgattccc ttcactgtgt gaatgttttc tgttgaaaaa atggaggata aatatggata 480
ctaatgacac tcattcctaa ttaagttttc aatcagtttg atttggataa cttgcattta 540
tccgagatat tgagctactt tctgataatg catcaagcat ttctaccata actctttcac 600
gcaactgaat gttgttaagt atagttttat cttgctttaa ttaaacttct taagcaaaaa 660
aaaagaaact tcataagcta atacattaga gaaaggttat gatcttgaat cnagaatggc 720
ttatggcatt aaggaatgag atacttgtaa attttctttg aaacagccaa ctcctctgtt 780
gtgtcttcac aattcaaaag atatgcctca ctgt 814

<210> 7
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
ccataactct ttcacgcaac tg 22

<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
acaacagagg agttggctgt tt 22

<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
ggtattgctg gctggtatct tt 22

<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
atgtaggaat agccgtggtg at 22

<210> 11
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
ggtctttgtg ttccagctct tc 22

<210> 12
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
ttctcaggac cagatagaga acg 23

<210> 13
<211> 483
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Clone S231
from BMEC from swine brain

<220>
<221> CDS
<222> (1)..(480)

<400> 13
atg ttg gtg tta ctg gct ggt atc ttt gtg gtc cac atc gcc act gtc 48
Met Leu Val Leu Leu Ala Gly Ile Phe Val Val His Ile Ala Thr Val
1 5 10 15

gtc atg ctg ttc gtt tgc acc att gcc aat gtc tgg gtg gtc tca gat 96
Val Met Leu Phe Val Cys Thr Ile Ala Asn Val Trp Val Val Ser Asp
20 25 30

gcg gga caa gga tct gtc ggt ctt tgg aaa aac tgt acc agt gct ggc 144
Ala Gly Gln Gly Ser Val Gly Leu Trp Lys Asn Cys Thr Ser Ala Gly
35 40 45

tgt act gat acc ctg tta tac ggc ggt gaa gat gcc ctc aag tcg gtg 192
Cys Thr Asp Thr Leu Leu Tyr Gly Gly Glu Asp Ala Leu Lys Ser Val
50 55 60

cag gcc ttc atg atc ctg tct atc atc ttc tct gtc gtc tcc ctc gtg 240
Gln Ala Phe Met Ile Leu Ser Ile Ile Phe Ser Val Val Ser Leu Val
65 70 75 80

```
gtc ttt gtg ttc cag ctc ttc acc atg gag aaa ggc aac cgc ttc ttc   288
Val Phe Val Phe Gln Leu Phe Thr Met Glu Lys Gly Asn Arg Phe Phe
                85                  90                  95

ctc tcg gga gcc acc atg ctg gtg tgc tgg ctg tgc atc atg gtg ggg   336
Leu Ser Gly Ala Thr Met Leu Val Cys Trp Leu Cys Ile Met Val Gly
            100                 105                 110

gcc tcc gtc tat act cat cat tat gcc aac agt tct aaa aac caa tac   384
Ala Ser Val Tyr Thr His His Tyr Ala Asn Ser Ser Lys Asn Gln Tyr
        115                 120                 125

tcg gcg agt cac cat ggc tat tcc ttc atc ctc gcc tgg atc tgc ttc   432
Ser Ala Ser His His Gly Tyr Ser Phe Ile Leu Ala Trp Ile Cys Phe
    130                 135                 140

tgc ttc agc ttc atc atc ggc gtt ctc tat ctg gtc ctg aga aag aaa   480
Cys Phe Ser Phe Ile Ile Gly Val Leu Tyr Leu Val Leu Arg Lys Lys
145                 150                 155                 160

taa                                                               483
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<210> 14
<211> 160
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Clone S231
from BMEC from swine brain

<400> 14

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Met Leu Val Leu Leu Ala Gly Ile Phe Val Val His Ile Ala Thr Val
  1               5                  10                  15

Val Met Leu Phe Val Cys Thr Ile Ala Asn Val Trp Val Val Ser Asp
            20                  25                  30

Ala Gly Gln Gly Ser Val Gly Leu Trp Lys Asn Cys Thr Ser Ala Gly
        35                  40                  45

Cys Thr Asp Thr Leu Leu Tyr Gly Gly Glu Asp Ala Leu Lys Ser Val
    50                  55                  60

Gln Ala Phe Met Ile Leu Ser Ile Ile Phe Ser Val Val Ser Leu Val
65                  70                  75                  80

Val Phe Val Phe Gln Leu Phe Thr Met Glu Lys Gly Asn Arg Phe Phe
                85                  90                  95

Leu Ser Gly Ala Thr Met Leu Val Cys Trp Leu Cys Ile Met Val Gly
            100                 105                 110

Ala Ser Val Tyr Thr His His Tyr Ala Asn Ser Ser Lys Asn Gln Tyr
        115                 120                 125

Ser Ala Ser His His Gly Tyr Ser Phe Ile Leu Ala Trp Ile Cys Phe
    130                 135                 140

Cys Phe Ser Phe Ile Ile Gly Val Leu Tyr Leu Val Leu Arg Lys Lys
145                 150                 155                 160
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<210> 15
<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Clone S012
from BMEC from swine brain

<400> 15
acatagaatt caatcaagtg taattcagaa taatgtgtat attagcatat ttacagtaat 60
gggatgtcat cgctattgtt agaatactga catcactttt ctgagcagaa attgaaactg 120
taaatttaac cttttaatta tcacctcacc tgaaaaggtt ggttgagata ctcacgcagc 180
atgtattata ttaaccatgt catgtttaag ttattaaatt cagattattt ataacttatt 240
atcttagggc ctgcctcatg tcttctaggg tatttgagta atcatcctat atttaaagtt 300
aaaactttga cttaaaaaac actgttaatg aaagttccct agcgcttttc ttattttcaa 360
attggtctta tgggtagtag tagagaattc catgctgttc tgaggctagc ttccaggtaa 420
acagtgattt ttttttttctt tttttctttc tttcttggtg agtggtccag agttttaagc 480
tacttttctc aaagtttcaa ccctttccca ggt 513

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
gtatcgggag tggaggatta ca 22

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
cccgaggtat atttgtttct gg 22

<210> 18
<211> 1674
<212> DNA
<213> Swine

<220>
<221> CDS
<222> (40)..(774)

<400> 18
ccgtctgcct ggtcccarag gcgcaccggc ttcggtaac atg ttt gtg gca gct 54
Met Phe Val Ala Ala
1 5

cgg aca ggc cag aga acc ttg aga aag gtg gtc tcg gga tgc cgt cca 102
Arg Thr Gly Gln Arg Thr Leu Arg Lys Val Val Ser Gly Cys Arg Pro
10 15 20

aaa tcg gcg aca gcg act gga gtc ccg gct cct gcg cag ggg cct ccg 150
Lys Ser Ala Thr Ala Thr Gly Val Pro Ala Pro Ala Gln Gly Pro Pro
25 30 35

cgg aac atc aga tac tta gcc tcc tgt ggt ata ctg atg aac aga act 198
Arg Asn Ile Arg Tyr Leu Ala Ser Cys Gly Ile Leu Met Asn Arg Thr
40 45 50

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ctt cca ctg cat tcc tca ttt ttg cct aag gag atg tat gca aga acc   246
Leu Pro Leu His Ser Ser Phe Leu Pro Lys Glu Met Tyr Ala Arg Thr
     55                  60                  65

ttc ttc aga att gct gca cca tta ata aac aaa aga aaa gaa tat tca   294
Phe Phe Arg Ile Ala Ala Pro Leu Ile Asn Lys Arg Lys Glu Tyr Ser
 70                  75                  80                  85

gag agg agg att ata gga tat tct atg cag gaa atg tat gac gta gta   342
Glu Arg Arg Ile Ile Gly Tyr Ser Met Gln Glu Met Tyr Asp Val Val
                 90                  95                 100

tcg gga atg gaa gat tac aag cat ttt gtg cct tgg tgc aaa aaa tca   390
Ser Gly Met Glu Asp Tyr Lys His Phe Val Pro Trp Cys Lys Lys Ser
            105                 110                 115

gat gta ata tca agg aga tct gga tac tgc aaa aca cga tta gaa att   438
Asp Val Ile Ser Arg Arg Ser Gly Tyr Cys Lys Thr Arg Leu Glu Ile
        120                 125                 130

ggg ttt cca ccc gta ttg gag cgc tat acg tca gta gta acc ttg gtg   486
Gly Phe Pro Pro Val Leu Glu Arg Tyr Thr Ser Val Val Thr Leu Val
    135                 140                 145

aaa cca cat ttg gta aag gca tcc tgt gca gat ggg aag ctc ttt aat   534
Lys Pro His Leu Val Lys Ala Ser Cys Ala Asp Gly Lys Leu Phe Asn
150                 155                 160                 165

cac tta gag act gtt tgg cgt ttt agc cca ggt ctt cct ggc tac cca   582
His Leu Glu Thr Val Trp Arg Phe Ser Pro Gly Leu Pro Gly Tyr Pro
                170                 175                 180

aga act tgt act ttg gat ttt tca att tct ttt gaa ttt cga tca ctt   630
Arg Thr Cys Thr Leu Asp Phe Ser Ile Ser Phe Glu Phe Arg Ser Leu
            185                 190                 195

ctg cac tct cag ctt gcc aca ttg ttt ttt gat gaa gtt gtg aag cag   678
Leu His Ser Gln Leu Ala Thr Leu Phe Phe Asp Glu Val Val Lys Gln
        200                 205                 210

atg gta gct gct ttt gaa aga aga gca tgt aaa ctg tat ggt cca gaa   726
Met Val Ala Ala Phe Glu Arg Arg Ala Cys Lys Leu Tyr Gly Pro Glu
    215                 220                 225

aca agt ata cct cgg gaa tta atg ctt cat gaa gtt cat cac aca taa   774
Thr Ser Ile Pro Arg Glu Leu Met Leu His Glu Val His His Thr
230                 235                 240                 245

gagaaaagga aatggttgcc tacttgtaac tagtttattc acttttagga agtgctttca 834

tcattttgct ytcagaaggc agaaagcatt tgtcaaacac agctttgata taaacctgta 894

ctttgcactt ggaatatgga accacatgta catagaattc aatcaagtgt aattcagaat 954

aatgtgtata ttagcatatt tacagtaatg ggatgtcatc gctattgtta gaatactgac 1014

atcacttttc tgagcagaaa ttgaaactgt aaatttaacc ttttaattat cacctcacct 1074

gaaaaggttg gttgagatac tcacgcagca tgtattatat taaccatgtc atgtttaagt 1134

tattaaattc agattattta taacttatta tcttagggcc tgcctcatgt cttctagggt 1194

atttgagtaa tcatcctata tttaaagtta aaactttgac ttaaaaaaca ctgttaatga 1254

aagttcccta gcgcttttct tattttcaaa ttggtcttat gggtagtagt agagaattcc 1314

atgctgttct gaggctagct tccaggtaaa cagtgatttt ttttttcttt ttttctttct 1374
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ttcttggtga gtggtccaga gttttaagct acttttctca aagtttcaac cctttcccag 1434

gtactttgac tactatttca gtaatgttga ttgtgtgtca agttttgtct acagcagtgg 1494

gcaatagatg aaggaagtcg gttgatatgt ctccaacacc atgcattctg attttctatt 1554

tattgtgtat actcactttc aataatgtat ttccaactga tatttttgta aacaaatcag 1614

tgtaaggact gaagtggtaa cttaataaag ttaatttgtt taaaaaataa aaaaaaaaaa 1674

<210> 19
<211> 244
<212> PRT
<213> Swine

<400> 19

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Met Phe Val Ala Ala Arg Thr Gly Gln Arg Thr Leu Arg Lys Val Val
  1               5                  10                  15
Ser Gly Cys Arg Pro Lys Ser Ala Thr Ala Thr Gly Val Pro Ala Pro
            20                  25                  30
Ala Gln Gly Pro Pro Arg Asn Ile Arg Tyr Leu Ala Ser Cys Gly Ile
        35                  40                  45
Leu Met Asn Arg Thr Leu Pro Leu His Ser Ser Phe Leu Pro Lys Glu
    50                  55                  60
Met Tyr Ala Arg Thr Phe Phe Arg Ile Ala Ala Pro Leu Ile Asn Lys
65                  70                  75                  80
Arg Lys Glu Tyr Ser Glu Arg Arg Ile Ile Gly Tyr Ser Met Gln Glu
                85                  90                  95
Met Tyr Asp Val Val Ser Gly Met Glu Asp Tyr Lys His Phe Val Pro
            100                 105                 110
Trp Cys Lys Lys Ser Asp Val Ile Ser Arg Arg Ser Gly Tyr Cys Lys
        115                 120                 125
Thr Arg Leu Glu Ile Gly Phe Pro Pro Val Leu Glu Arg Tyr Thr Ser
    130                 135                 140
Val Val Thr Leu Val Lys Pro His Leu Val Lys Ala Ser Cys Ala Asp
145                 150                 155                 160
Gly Lys Leu Phe Asn His Leu Glu Thr Val Trp Arg Phe Ser Pro Gly
                165                 170                 175
Leu Pro Gly Tyr Pro Arg Thr Cys Thr Leu Asp Phe Ser Ile Ser Phe
            180                 185                 190
Glu Phe Arg Ser Leu Leu His Ser Gln Leu Ala Thr Leu Phe Phe Asp
        195                 200                 205
Glu Val Val Lys Gln Met Val Ala Ala Phe Glu Arg Arg Ala Cys Lys
    210                 215                 220
Leu Tyr Gly Pro Glu Thr Ser Ile Pro Arg Glu Leu Met Leu His Glu
225                 230                 235                 240
Val His His Thr
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<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
cgcgtggtga atgatctgta 20

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
ctccatgatc aggtcctcca g 21

<210> 22
<211> 607
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Partial
CDNA sequence of NSE2 from swine

<220>
<221> CDS
<222> (1)..(192)

<400> 22
gag gac ctg atc atg gag aaa cgg cgc aac gac cag ata ggg cgc gcc 48
Glu Asp Leu Ile Met Glu Lys Arg Arg Asn Asp Gln Ile Gly Arg Ala
1 5 10 15

gcg gtg cta cag gag ctg gcc acg cac ctg cac ccc gcg gag ccg gac 96
Ala Val Leu Gln Glu Leu Ala Thr His Leu His Pro Ala Glu Pro Asp
20 25 30

gag ggc gac agc gac gcc gcg cgg act acg ccg cct ccc ggg cgc tcc 144
Glu Gly Asp Ser Asp Ala Ala Arg Thr Thr Pro Pro Pro Gly Arg Ser
35 40 45

cag gcg ccg ggc caa gag gag gag gac cga gag gcg gtg gtg cac tga 192
Gln Ala Pro Gly Gln Glu Glu Glu Asp Arg Glu Ala Val Val His
50 55 60

caggcgagct gagtgcggag ctgcgtgagg gagcctttgc agcagccgct gccccctccc 252

ttctctccct ccctcctcca ccatcttctg ggtcccaact gggctcctgg gccatttgga 312

aaacggagag ttggcgaaaa gcgctgccag ctgtggcttg agtttgttat cttggacgga 372

ggaggaagag ggagcagctt ccatggaccc ctgatcacta cttgaggaga attttcctgt 432

ggattcaact gactagctat tgtgatgtaa gcagtttgag gtgactggcc cagcaggagt 492

gagaagaatt tatcttcagc ataaacttca ttattctaca gtgtttcttc atttgcctga 552

gaggtaagga tgctatgtag acagaaacaa aggaagaaaa aaaaaaaaaa aaaaa 607

<210> 23
<211> 63
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Partial
CDNA sequence of NSE2 from swine

<400> 23
Glu Asp Leu Ile Met Glu Lys Arg Arg Asn Asp Gln Ile Gly Arg Ala
1 5 10 15
Ala Val Leu Gln Glu Leu Ala Thr His Leu His Pro Ala Glu Pro Asp
20 25 30
Glu Gly Asp Ser Asp Ala Ala Arg Thr Thr Pro Pro Pro Gly Arg Ser
35 40 45
Gln Ala Pro Gly Gln Glu Glu Glu Asp Arg Glu Ala Val Val His
50 55 60

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
cgagaccctg tggtggctta ttac 24

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
ctggtgtatt agctggagcg tgtg 24

<210> 26
<211> 586
<212> DNA
<213> Swine

<220>
<221> CDS
<222> (1)..(585)

<400> 26

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cga gac cct gtg gtg gct tat tac tgt cgt tta tat gca atg caa act   48
Arg Asp Pro Val Val Ala Tyr Tyr Cys Arg Leu Tyr Ala Met Gln Thr
  1               5                  10                  15

gga atg aag att gat agt aaa act cct gaa tgt cgt aaa ttt tta tca   96
Gly Met Lys Ile Asp Ser Lys Thr Pro Glu Cys Arg Lys Phe Leu Ser
            20                  25                  30

aag ctg atg gat cag tta gaa gct ctt aag aaa cag ttg ggt gac aat   144
Lys Leu Met Asp Gln Leu Glu Ala Leu Lys Lys Gln Leu Gly Asp Asn
        35                  40                  45

gaa gct gtt act caa gaa ata gtt ggt tct gcc cac ttg gag aat tat   192
Glu Ala Val Thr Gln Glu Ile Val Gly Ser Ala His Leu Glu Asn Tyr
    50                  55                  60

gct ttg aaa atg ttt tta tat gca gat aat gaa gat cgg gct ggg cga   240
Ala Leu Lys Met Phe Leu Tyr Ala Asp Asn Glu Asp Arg Ala Gly Arg
65                  70                  75                  80

ttt cat aaa aac atg atc aag tcc ttc tat act gca agt ctt tta ata   288
Phe His Lys Asn Met Ile Lys Ser Phe Tyr Thr Ala Ser Leu Leu Ile
                85                  90                  95

gat gtc ata aca gtg ttt gga gaa ctc act gat gaa aat gtg aaa cac   336
Asp Val Ile Thr Val Phe Gly Glu Leu Thr Asp Glu Asn Val Lys His
            100                 105                 110

aga aag tat gca agg tgg aag gca aca tat att cat aat tgt tta aag   384
Arg Lys Tyr Ala Arg Trp Lys Ala Thr Tyr Ile His Asn Cys Leu Lys
        115                 120                 125
```

```
aat gga ggg act cct caa gca ggt cct gtg ggc att gaa gaa gat aat   432
Asn Gly Gly Thr Pro Gln Ala Gly Pro Val Gly Ile Glu Glu Asp Asn
    130                 135                 140

gac ata gaa gaa aat gaa gat gct gga gca acc tct ctg ccc act cag   480
Asp Ile Glu Glu Asn Glu Asp Ala Gly Ala Thr Ser Leu Pro Thr Gln
145                 150                 155                 160

cca cct cag cca tca tct tcc act tat gac cca ggc aac atg cca tcg   528
Pro Pro Gln Pro Ser Ser Ser Thr Tyr Asp Pro Gly Asn Met Pro Ser
                165                 170                 175

agc agc tat act gga ata cag att cct ccc ggt gca cac gct cca gct   576
Ser Ser Tyr Thr Gly Ile Gln Ile Pro Pro Gly Ala His Ala Pro Ala
            180                 185                 190

aat aca cca g                                                    586
Asn Thr Pro
        195
```

<210> 27
<211> 195
<212> PRT
<213> Swine

<400> 27

```
Arg Asp Pro Val Val Ala Tyr Tyr Cys Arg Leu Tyr Ala Met Gln Thr
  1               5                  10                  15

Gly Met Lys Ile Asp Ser Lys Thr Pro Glu Cys Arg Lys Phe Leu Ser
            20                  25                  30

Lys Leu Met Asp Gln Leu Glu Ala Leu Lys Lys Gln Leu Gly Asp Asn
        35                  40                  45

Glu Ala Val Thr Gln Glu Ile Val Gly Ser Ala His Leu Glu Asn Tyr
    50                  55                  60

Ala Leu Lys Met Phe Leu Tyr Ala Asp Asn Glu Asp Arg Ala Gly Arg
65                  70                  75                  80

Phe His Lys Asn Met Ile Lys Ser Phe Tyr Thr Ala Ser Leu Leu Ile
                85                  90                  95

Asp Val Ile Thr Val Phe Gly Glu Leu Thr Asp Glu Asn Val Lys His
            100                 105                 110

Arg Lys Tyr Ala Arg Trp Lys Ala Thr Tyr Ile His Asn Cys Leu Lys
        115                 120                 125

Asn Gly Gly Thr Pro Gln Ala Gly Pro Val Gly Ile Glu Glu Asp Asn
    130                 135                 140

Asp Ile Glu Glu Asn Glu Asp Ala Gly Ala Thr Ser Leu Pro Thr Gln
145                 150                 155                 160

Pro Pro Gln Pro Ser Ser Ser Thr Tyr Asp Pro Gly Asn Met Pro Ser
                165                 170                 175

Ser Ser Tyr Thr Gly Ile Gln Ile Pro Pro Gly Ala His Ala Pro Ala
            180                 185                 190

Asn Thr Pro
        195
```

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 28
aaaaggcccc cagggttacg 20

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 29
ggagtgggca gcaggtgagc 20

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 30
ttaacctgca cagcgacaag t 21

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
ttgctgaaga tctcacgctt c 21

<210> 32
<211> 1194
<212> DNA
<213> Swine

<220>
<221> CDS
<222> (1)..(741)

<400> 32
acg gac gag gag ctc cgc agg cgc cag ctg act tgc acc gag gag atg 48
Thr Asp Glu Glu Leu Arg Arg Arg Gln Leu Thr Cys Thr Glu Glu Met
1 5 10 15

gcc cag cga ggg ctg ccg cct gcc ctt gac ccc tgg gag ccg aag gcg 96
Ala Gln Arg Gly Leu Pro Pro Ala Leu Asp Pro Trp Glu Pro Lys Ala
20 25 30

```
gac tgg gcg ccc gca ggc agc ctc agc ggt gag gcc ggc cag aag gat   144
Asp Trp Ala Pro Ala Gly Ser Leu Ser Gly Glu Ala Gly Gln Lys Asp
          35                  40                  45

gtc aac ggg ccc ctg agg gag ctg cgc cca agg ctc tgc cac ctg cga   192
Val Asn Gly Pro Leu Arg Glu Leu Arg Pro Arg Leu Cys His Leu Arg
      50                  55                  60

aaa ggc ccc cag ggt tac ggg ttt aac ctg cac agc gac aag tcc cgg   240
Lys Gly Pro Gln Gly Tyr Gly Phe Asn Leu His Ser Asp Lys Ser Arg
 65                  70                  75                  80

cct gga cag tac atc cgc tcc gtg gac cca ggc tca cct gct gcc cac   288
Pro Gly Gln Tyr Ile Arg Ser Val Asp Pro Gly Ser Pro Ala Ala His
                 85                  90                  95

tcc ggc ctc cga gcc cag gac cga ctc ata gag gtg aac ggg cag aat   336
Ser Gly Leu Arg Ala Gln Asp Arg Leu Ile Glu Val Asn Gly Gln Asn
            100                 105                 110

gtg gag ggg ctg cgg cac gcg gag gtg gtt gcc tgc atc aag gcg cgg   384
Val Glu Gly Leu Arg His Ala Glu Val Val Ala Cys Ile Lys Ala Arg
        115                 120                 125

gag gac gag gcc cgg ctg ctg gtg gtg gac ccc gag acg gat gtg tac   432
Glu Asp Glu Ala Arg Leu Leu Val Val Asp Pro Glu Thr Asp Val Tyr
    130                 135                 140

ttc aag cgg ctg cgg gtc aca ccc acc cag gag cac atg gaa ggt cca   480
Phe Lys Arg Leu Arg Val Thr Pro Thr Gln Glu His Met Glu Gly Pro
145                 150                 155                 160

ctg tca tca cct gtc acc aat ggg acc agc tca gcc cag ctc aat ggt   528
Leu Ser Ser Pro Val Thr Asn Gly Thr Ser Ser Ala Gln Leu Asn Gly
                165                 170                 175

ggc tcc gtg tgc tcg tcc cga agt gac ctg ccc ggc tta gac aag gac   576
Gly Ser Val Cys Ser Ser Arg Ser Asp Leu Pro Gly Leu Asp Lys Asp
            180                 185                 190

act gag gac agc agc acc tgg aag cgt gac cct ttc cag gag agt ggc   624
Thr Glu Asp Ser Ser Thr Trp Lys Arg Asp Pro Phe Gln Glu Ser Gly
        195                 200                 205

ctc cac ctg agc ccc acg gcg gct ggg gcc aag gag aag gcg agg gcc   672
Leu His Leu Ser Pro Thr Ala Ala Gly Ala Lys Glu Lys Ala Arg Ala
    210                 215                 220

acc agg gtc aac aag cgg gcg cca cag atg gac tgg aac cgg aag cgt   720
Thr Arg Val Asn Lys Arg Ala Pro Gln Met Asp Trp Asn Arg Lys Arg
225                 230                 235                 240

gag atc ttc agc aac ttc tga gacccccac cctccgccgc agccgccgcc       771
Glu Ile Phe Ser Asn Phe
                245
```

```
tggtccccag ccgggcctcc tctgggcatg gaccttgggc cttgcccaga gcgccccgag 831

cctcagtgga ctgcagcggg ggcaccttcg ctcgctaagc cgtggtggtc ccaccacccc 891

ccatgaacca gcccgtgccc cagtgagccc ccgtcctgcc cccttcccac ggggtgctgg 951

ggagcgggca gaggaagccc ctgagacggg agggacagag acacccagag aggtgggctg 1011

gggaggggag gttggggtga cccgccaggc cgggcccttg ctgctctgcc tgggcctgct 1071

gacttaaagg aatttgtgtt ttggcttttt ttccaacacg agctctggct ccacacatgt 1131
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ttccacttaa taccagagcc cccaccccca tcccctcagg acgtgctctc taaataattg 1191

caa 1194

<210> 33
<211> 246
<212> PRT
<213> Swine

<400> 33

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Thr Asp Glu Glu Leu Arg Arg Arg Gln Leu Thr Cys Thr Glu Glu Met
  1               5                  10                  15
Ala Gln Arg Gly Leu Pro Pro Ala Leu Asp Pro Trp Glu Pro Lys Ala
            20                  25                  30
Asp Trp Ala Pro Ala Gly Ser Leu Ser Gly Glu Ala Gly Gln Lys Asp
        35                  40                  45
Val Asn Gly Pro Leu Arg Glu Leu Arg Pro Arg Leu Cys His Leu Arg
    50                  55                  60
Lys Gly Pro Gln Gly Tyr Gly Phe Asn Leu His Ser Asp Lys Ser Arg
65                  70                  75                  80
Pro Gly Gln Tyr Ile Arg Ser Val Asp Pro Gly Ser Pro Ala Ala His
                85                  90                  95
Ser Gly Leu Arg Ala Gln Asp Arg Leu Ile Glu Val Asn Gly Gln Asn
            100                 105                 110
Val Glu Gly Leu Arg His Ala Glu Val Val Ala Cys Ile Lys Ala Arg
        115                 120                 125
Glu Asp Glu Ala Arg Leu Leu Val Val Asp Pro Glu Thr Asp Val Tyr
    130                 135                 140
Phe Lys Arg Leu Arg Val Thr Pro Thr Gln Glu His Met Glu Gly Pro
145                 150                 155                 160
Leu Ser Ser Pro Val Thr Asn Gly Thr Ser Ser Ala Gln Leu Asn Gly
                165                 170                 175
Gly Ser Val Cys Ser Ser Arg Ser Asp Leu Pro Gly Leu Asp Lys Asp
            180                 185                 190
Thr Glu Asp Ser Ser Thr Trp Lys Arg Asp Pro Phe Gln Glu Ser Gly
        195                 200                 205
Leu His Leu Ser Pro Thr Ala Ala Gly Ala Lys Glu Lys Ala Arg Ala
    210                 215                 220
Thr Arg Val Asn Lys Arg Ala Pro Gln Met Asp Trp Asn Arg Lys Arg
225                 230                 235                 240
Glu Ile Phe Ser Asn Phe
                245
```

<210> 34
<211> 63
<212> PRT
<213> Swine

<400> 34

```
Glu Asp Leu Ile Met Glu Lys Arg Arg Asn Asp Gln Ile Gly Arg Ala
  1               5                  10                  15
Ala Val Leu Gln Glu Leu Ala Thr His Leu His Pro Ala Glu Pro Asp
            20                  25                  30
Glu Gly Asp Ser Asp Ala Ala Arg Thr Thr Pro Pro Pro Gly Arg Ser
        35                  40                  45
Gln Ala Pro Gly Gln Glu Glu Glu Asp Arg Glu Ala Val Val His
    50                  55                  60
```

<210> 35
<211> 367
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Clone S064
from BMEC from swine brain

<400> 35
acaataccag gggtccccca gagagatcct gttcataatt ttgtcctttt taacaccatt 60
tcatttgatc aagctgatta gctaagatct tgttacagca tttgcagaaa gcctgaagct 120
tgatggataa caacagtttt aaaccttaag aaatgacaag tataaataca gacacttcaa 180
tgtagtttta cattctgagg caagaaatat attatacagg gcctgctgtt tcctctttaa 240
tgctctaaaa gcaccaattt atgttaaaga tggcaatgtg taattataat cattataatc 300
tgattagacc aaacacagga gcaaagctgt aattgctttt agtttttgtt tttttaacat 360
gctctgt 367

<210> 36
<211> 3071
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Clone S064.3
from BMEC from swine brain

<400> 36
sctwtggcgg ggwatctcwa ggacaaatww waatggaatw atctctggct ggcactcatt 60
taattcttaa ctatgtaaaa caacatgagt agaaaaaaat ttagtggtat tatgcctaga 120
atagataggt gaattccatt gatgtttatc tttgaagacc agctttatgc gtgaactttt 180
catctgwggc tttggatcca aaacatttca tgtccagttc agttctaaag gttcttttat 240
attttgtcag ggtagtctct ttgagataca gcatgatgac ttgaatctag cagaatattg 300
tgctggctac ctaaagaagt gggttcaaat cttaatttgg ccattacctt ttgaccttag 360
acagttacta ctgtttatgg tcttccttct gtttttccca tgcagaggaa cttaaacaaa 420
ttatagagtg ccaacatgtc tcttggtttt aaaatcgtga atctattaaa atcccgaatc 480
tactaaaaca ctattaaaaa ctggaaaaaa aattcaacta gggaaagaca tgtaatatga 540
aatttatttt tacctatcat ttgattccca ctttattatc ytttcattta gtatatgaat 600
acaatccaat aagaaaatga aggtcaacta ctgccactcc acttaaattg aactaatagt 660
taatgaagtg caaaagagaa aataagccat attgctaaga agatgatata ttaagctgct 720
gataaaatac cagtgtgtgt tgaaaatact cttttagaag ataccttgct tattttcctg 780
gcttttatta attggatgga aatggttagt ttgatcagag tttattggct ctagaggctg 840
ccccaaattg tagctctgtt tgactttcca gtattgaaag aatactggaa atgtcaatat 900
tttacaaatg tctgtacaaa tctgaaagta gtttatatcc atggttagtt ttttcagtaa 960
cgttccatcc ttattcattt agcattactg taaagccagg ttcccaagaa gtattttcta 1020
agagttccaa gtaaccacag ctacatagag aaagccaata aaaacaaaac tttttagcta 1080
cttctctgta aatttaaagt agaaaaaaac cagacctaaa gtcagctttr aatgtatgtg 1140
gtctagtgaa atgtttggga aatgtttatt tggaggttta gaggcatacc gaagcaggag 1200
tcaaaacaaa gttggtggta aagattaaca tgaagtaaaa aaatcttcag tagaaaatag 1260
aaagtttgaa tgaaaacaat gagttgtccc cattcaaggc acttaaaatw actagaaaat 1320
tctgtctttt actgtaattg gatggcctat attatttcta atgtggccaa aggactaaag 1380
accaatcagg tttctagaat tggggagcgt agtcacatag aggcatcttt tgcatttttt 1440
aannnaccag taatcttcct tttcccctta gaaakggaga aataaaatgt tctgtacata 1500
tcttttggaa tagaaagcaa aattctagaa gaatggaagt atcctcttac accaacttgt 1560
agttttaatt gaaaaattac ctcatttttc agtccatacg gtgctttgct cgagtttgtg 1620
gaatggtcca ccatcccatt aaaacccgct tcacccaagc tgtatttcaa atatgcaaaa 1680
ttcacagcta agggatagca gtccttggag gttttgtttt ccttcactcg cgcttaccac 1740
cagcagagct aataacgtga tgtaccaggt tgacatactg cttcattaaa gcacatgggc 1800
aagtgtttag tcaatattta attagtttaa ttaaaatcaa ataagggaaa ggaaaaaccc 1860
ttaagtttga ttgagttaca ttatactgtg aatatatttc catctgtgtt gataagacat 1920
caaatgacta tcagttgata ttgattatac ataatttatt tgcatattct ggccctattc 1980
atgagaggct ataatcattt taatcttaca ttttccttca ggaaattcag ggactctaca 2040
gcccctattt tgttctcttg gagtaaawtg ttcagtgtag tttatgaaaa cttttcattt 2100
tggttttaaa aaaggcttag ctgctagttc attaaaagtg tgaaataaaa tgatggttat 2160
gatttttcca attaatgtta taaattttas cstrtycrtc yrwkgtacag agcatgttaa 2220
aaaaacaaaa actaaaagca attacagctt tgctcctgtg tttggtctaa tcagattata 2280
atgattataa ttacacattg ccatcttaac ataaattggt gcttttagag cattaaagag 2340
gaaacagcag gccctgtata atatatttct tgcctcagaa tgtaaaacta cattgaagtg 2400
tctgtattta tacttgtcat ttcttaaggt ttaaaactgt tgttatccat caagcttcag 2460
gctttctgca aatgctgtaa caagatctta gctaatcagc ttgrtcaaat gaaatggtgt 2520

taaaaaggac aaaattatga acaggatctc tctgggggac ccctggtatt gtacmkrmss 2580
gggsggaacy gtctykmatg ccacaaactg tgcgtcataa tcccacccaa acaactgaca 2640
tgtgtgtwat tggttcaata cataagcatt aataaaatta aaggaacaaa ttacttaaag 2700
cagtcacatc atcacttcct caaagtggtt yaaagcatgt tcttctaaat ggtggagttg 2760
tttaaagaca tgttttaaat tttgatagct ttactactgt cataaaatgc ttctatatgt 2820
taagtttagg ttgctggtac tcatgatttt ttacttctgc aattatgctg taatgagttg 2880
cttgcatgcc tacttaccca agtgaaagga tgctgtttgc tctggaatgt tcatctttta 2940
gacaggtttk sgctcatttg caatcatggt gcaatacagt gtaacattca tttgttttca 3000
gtcaatagtt ttatttttgt cmcaataaat aattactttt ccaaaaaaaa aaaaaaaaaa 3060
aaaaaaaaaa a 3071

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 37
taatgcaggg aaaaccacca ttct 24

<210> 38
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 38
aaccaagaga catgttggca ct 22

<210> 39
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 39
atagcattga cagggaacga ct 22

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial sequence: Primer

<400> 40
ctgctagatt caagtcatca tgc 23

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 41
ctcgtgatgg ggctgatctt c 21

<210> 42
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 42
atctcacacc aatccgggag gt 22

<210> 43
<211> 540
<212> DNA
<213> Swine

<220>
<221> CDS
<222> (1)..(537)

<400> 43
atg ggg ctg atc ttc gct aaa ctg tgg agc ctc ttc tgt aac caa gag 48
Met Gly Leu Ile Phe Ala Lys Leu Trp Ser Leu Phe Cys Asn Gln Glu
1 5 10 15

cac aaa gta att ata gtg gga ctg gat aac gca ggg aag acc act att 96
His Lys Val Ile Ile Val Gly Leu Asp Asn Ala Gly Lys Thr Thr Ile
20 25 30

ctt tat cag ttc tta atg aat gaa gtg gtt cat aca tct cca act ata 144
Leu Tyr Gln Phe Leu Met Asn Glu Val Val His Thr Ser Pro Thr Ile
35 40 45

gga agc aat gtt gaa gaa ata gtt gtg aag aac act cat ttt ctc atg 192
Gly Ser Asn Val Glu Glu Ile Val Val Lys Asn Thr His Phe Leu Met
50 55 60

tgg gat att ggt ggt caa gag tca ctg cgg tca tcc tgg aac acg tat 240
Trp Asp Ile Gly Gly Gln Glu Ser Leu Arg Ser Ser Trp Asn Thr Tyr
65 70 75 80

tat tca aac aca gag ttc atc att ctt gtg gtt gat agc att gac agg 288
Tyr Ser Asn Thr Glu Phe Ile Ile Leu Val Val Asp Ser Ile Asp Arg
85 90 95

gaa cga cta gct att acg aaa gaa gaa tta tac aga atg ttg gct cat 336
Glu Arg Leu Ala Ile Thr Lys Glu Glu Leu Tyr Arg Met Leu Ala His
100 105 110

gag gat tta cgg aag gct gca gtc ctt atc ttt gcc aat aaa cag gat 384
Glu Asp Leu Arg Lys Ala Ala Val Leu Ile Phe Ala Asn Lys Gln Asp
115 120 125

atg aaa ggg tgc atg aca gca gct gaa atc tcc aaa tac ctc acc ctc 432
Met Lys Gly Cys Met Thr Ala Ala Glu Ile Ser Lys Tyr Leu Thr Leu
130 135 140

agt tca att aag gat cat ccg tgg cat att cag tcc tgc tgt gct tta 480
Ser Ser Ile Lys Asp His Pro Trp His Ile Gln Ser Cys Cys Ala Leu
145 150 155 160

aca gga gaa ggg tta tgc caa ggt cta gag tgg atg acc tcc cgg att 528
Thr Gly Glu Gly Leu Cys Gln Gly Leu Glu Trp Met Thr Ser Arg Ile
165 170 175

ggt gtg aga taa 540
Gly Val Arg

<210> 44
<211> 179
<212> PRT
<213> Swine

<400> 44
Met Gly Leu Ile Phe Ala Lys Leu Trp Ser Leu Phe Cys Asn Gln Glu
1 5 10 15

His Lys Val Ile Ile Val Gly Leu Asp Asn Ala Gly Lys Thr Thr Ile
20 25 30

Leu Tyr Gln Phe Leu Met Asn Glu Val Val His Thr Ser Pro Thr Ile
35 40 45

Gly Ser Asn Val Glu Glu Ile Val Val Lys Asn Thr His Phe Leu Met
50 55 60

Trp Asp Ile Gly Gly Gln Glu Ser Leu Arg Ser Ser Trp Asn Thr Tyr
65 70 75 80

Tyr Ser Asn Thr Glu Phe Ile Ile Leu Val Val Asp Ser Ile Asp Arg
85 90 95

Glu Arg Leu Ala Ile Thr Lys Glu Glu Leu Tyr Arg Met Leu Ala His
100 105 110

Glu Asp Leu Arg Lys Ala Ala Val Leu Ile Phe Ala Asn Lys Gln Asp
115 120 125

Met Lys Gly Cys Met Thr Ala Ala Glu Ile Ser Lys Tyr Leu Thr Leu
130 135 140

Ser Ser Ile Lys Asp His Pro Trp His Ile Gln Ser Cys Cys Ala Leu
145 150 155 160

Thr Gly Glu Gly Leu Cys Gln Gly Leu Glu Trp Met Thr Ser Arg Ile
165 170 175

Gly Val Arg

<210> 45
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 45
aagcctgaag cttgatggat aa 22

<210> 46
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 46
caattacagc tttgctcctg tg 22

<210> 47
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
atagcattga cagggaacga ct 22

<210> 48
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
gaactgaggg tgaggtattt gg 22

<210> 49
<211> 332
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Clone 5G9 from
BMEC from swine brain

<400> 49
agcggagggc gcgcccatca gcctgctccg cagggtccgg ggcgctcttt tcacctggaa 60
tattttgaaa acaattgccc tgggtcasat gttgtccttg ygtatatgtg ggacagccat 120
caccagccag tatttggcag aaaaatacaa agtgaatacg cccatgcttc agagctttat 180
caactattgc ttgctgtttc taatttatac aatgatgctg gcatttcagt caggtaataa 240
taacctttta tgcatcttga aaaagaaatg gtggaagtat atcctgctcg gactggcaga 300
tgtggaagct aattacctga ttgtcagagc gt 332

<210> 50
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 50
tgtatatgtg ggacagccat ca 22

<210> 51
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 51
gtccgagcag gatatacttc ca 22

<210> 52
<211> 2319
<212> DNA
<213> Swine

<220>
<221> CDS
<222> (480)..(1466)

<400> 52
agtctctctt cagtccacac aagcctcaga agggtggcct acgggttgga atcgcccctt 60

caatggcacc tcagagacat ctctgcatcg aaaggcaaac cgaacacgtc cttaaggagg 120

agacaccaca gaaacatgtt tccaggattc tttaaggacg ggaaagatag ggaagaaaag 180

aaacagaact ataggaaata ccttttacga tagtcaagag ggagggagac taggtccaag 240

gaggggtcag tcggtcctcc ccagttaaca aaggtcattg cttttcaggt ggcataacct 300

cgattcacct caggtgctga ttttagataa ggaaccgtaa gaacctgaac cgcctcttgg 360

gtgtctcctc accccacgca gaagccccac tgccaagacg aagaggaaga gggcatttct 420

cctccaactc ctgctccgga ggtgccagga atattttgaa aacaattgcc ctgggtcag 479

atg ttg tcc ttg tgt ata tgt ggg aca gcc atc acc agc cag tat ttg 527
Met Leu Ser Leu Cys Ile Cys Gly Thr Ala Ile Thr Ser Gln Tyr Leu
1 5 10 15

gca gaa aaa tac aaa gtg aat acg ccc atg ctt cag agc ttt atc aac 575
Ala Glu Lys Tyr Lys Val Asn Thr Pro Met Leu Gln Ser Phe Ile Asn
20 25 30

tat tgc ttg ctg ttt cta att tat aca atg atg ctg gca ttt cag tca 623
Tyr Cys Leu Leu Phe Leu Ile Tyr Thr Met Met Leu Ala Phe Gln Ser
35 40 45

ggt aat aat aac ctt tta tgc atc ttg aaa aag aaa tgk tgg aag tat 671
Gly Asn Asn Asn Leu Leu Cys Ile Leu Lys Lys Lys Xaa Trp Lys Tyr
50 55 60

atc ctg ctc gga ctg gca gat gtg gaa gct aat tac ctg att gtc aga 719
Ile Leu Leu Gly Leu Ala Asp Val Glu Ala Asn Tyr Leu Ile Val Arg
65 70 75 80

gcg tac cag tac aca act cta acc agt gtc cag ctt ttg gat tgc ttt 767
Ala Tyr Gln Tyr Thr Thr Leu Thr Ser Val Gln Leu Leu Asp Cys Phe
85 90 95

ggg att cct gtg ttg atg gct ctc tcg tgg ttt att ctt tat gca aga 815
Gly Ile Pro Val Leu Met Ala Leu Ser Trp Phe Ile Leu Tyr Ala Arg
100 105 110

tac aga gtg atc cac ttc atc gct gtg gct gtc tgt ctg ttg ggc gta 863
Tyr Arg Val Ile His Phe Ile Ala Val Ala Val Cys Leu Leu Gly Val
115 120 125

gga act atg gtt ggt gca gac ata tta gca ggg aga gaa gac aat tca 911
Gly Thr Met Val Gly Ala Asp Ile Leu Ala Gly Arg Glu Asp Asn Ser
130 135 140

ggt agt gat gtg ctg att ggt gac gtc ttg gtc ctt ctt ggg gcc tcc 959
Gly Ser Asp Val Leu Ile Gly Asp Val Leu Val Leu Leu Gly Ala Ser
145 150 155 160

ctc tat gca gtt tct aat gtg tgt gaa gaa tac atc gtg aag aag ctg 1007
Leu Tyr Ala Val Ser Asn Val Cys Glu Glu Tyr Ile Val Lys Lys Leu
165 170 175

agc cga cag gag ttt tta gga atg gtg ggc ttg ttt gga aca att atc 1055
Ser Arg Gln Glu Phe Leu Gly Met Val Gly Leu Phe Gly Thr Ile Ile
180 185 190

agt ggc ata cag cta ttg att gtg gaa tat aag gat att gcc agc att 1103
Ser Gly Ile Gln Leu Leu Ile Val Glu Tyr Lys Asp Ile Ala Ser Ile
195 200 205

cac tgg gac tgg aaa att gcc cta ctg ttt gta gca ttt gcc ctc tgt 1151
His Trp Asp Trp Lys Ile Ala Leu Leu Phe Val Ala Phe Ala Leu Cys
210 215 220

atg ttt tgc ctg tac agc ttc atg cca ctg gtg att aaa gtc act agt 1199
Met Phe Cys Leu Tyr Ser Phe Met Pro Leu Val Ile Lys Val Thr Ser
225 230 235 240

gcc act tct gtc aac ctg ggc atc ctg aca gct gac ctc tat agt ctt 1247
Ala Thr Ser Val Asn Leu Gly Ile Leu Thr Ala Asp Leu Tyr Ser Leu
245 250 255

ttc ttt gga ctc ttc ctg ttt ggc tat aag ttc tcg gga ctc tac atc 1295
Phe Phe Gly Leu Phe Leu Phe Gly Tyr Lys Phe Ser Gly Leu Tyr Ile
260 265 270

ctg tcc ttc gct gtc atc atg gtg ggg ttc att ctg tac tgt tcc acg 1343
Leu Ser Phe Ala Val Ile Met Val Gly Phe Ile Leu Tyr Cys Ser Thr
275 280 285

ccg acg cgc acg gca gag ccg gct gaa agc agc gtg cca cca cca gtc 1391
Pro Thr Arg Thr Ala Glu Pro Ala Glu Ser Ser Val Pro Pro Pro Val
290 295 300

acc agc atc ggg atc gac aac ctg ggc ctg aag ctt gag gag aac ctc 1439
Thr Ser Ile Gly Ile Asp Asn Leu Gly Leu Lys Leu Glu Glu Asn Leu
305 310 315 320

ccg gag acc cac tcc gtg gcc tta tag ctggagaaga aggcacacac 1486
Pro Glu Thr His Ser Val Ala Leu
325

atgtactgcg gctttctggg aagccgggag ctatcacctg aataaagcag agcctgttgc 1546

ctgctgaggg gacacttgga aaatgatcag atgcagagtg aacactctgg agcactggat 1606

tggctctagt ggttagattt tatgaaggaa tacaaatcaa tgtatcaaag gtagaagtac 1666

caaagtagag cagaagctaa ggcaaggatt gtgtttttgt gtgtttaggg accaatgtgt 1726

attaacgtca gggagacaag gtgtgaggcc cacactgggg tctcagaggc acaagatggg 1786

aaagcaggat ggggtggata ctcaggtgtg aggcagcctc aggacagggc ctgaaagcag 1846

gctgtccagg taggctggtt ggtcggggag gggaagagca tcccaggatg gtttgggatt 1906

aggtttgctc agttggaggc atctgagttc tgtcctgctg aggcagtgat tgtctcatgg 1966

gctagacgag gtctggtgac tgattgcgta catcaggaag atggagggtg cagcactgga 2026

gaaatcctga gatacaagtg tagaaccata gaagcagcac agcggatcct tctcccaatt 2086

gttactacac taatcttagc aaataatgtg ccatgagatt tttatgagac ttcttcaaaa 2146

caaagttaac aggaagcatc attatgatat caactaccaa gcagtatgcc mctttacaca 2206

gatgctctat gtaaattttg ggggggtaaa aatataataa aggaatcgag ggtaaatgtt 2266

catattatta aaaatttttg atttcataga aaaaaaaaaa aaaaaaaaaa aaa 2319

<210> 53
<211> 328
<212> PRT
<213> Swine

<400> 53

Met	Leu	Ser	Leu	Cys	Ile	Cys	Gly	Thr	Ala	Ile	Thr	Ser	Gln	Tyr	Leu
1				5					10					15	
Ala	Glu	Lys	Tyr	Lys	Val	Asn	Thr	Pro	Met	Leu	Gln	Ser	Phe	Ile	Asn
			20					25					30		
Tyr	Cys	Leu	Leu	Phe	Leu	Ile	Tyr	Thr	Met	Met	Leu	Ala	Phe	Gln	Ser
		35					40					45			
Gly	Asn	Asn	Asn	Leu	Leu	Cys	Ile	Leu	Lys	Lys	Lys	Xaa	Trp	Lys	Tyr
	50					55					60				
Ile	Leu	Leu	Gly	Leu	Ala	Asp	Val	Glu	Ala	Asn	Tyr	Leu	Ile	Val	Arg
65					70					75					80
Ala	Tyr	Gln	Tyr	Thr	Thr	Leu	Thr	Ser	Val	Gln	Leu	Leu	Asp	Cys	Phe
				85					90					95	
Gly	Ile	Pro	Val	Leu	Met	Ala	Leu	Ser	Trp	Phe	Ile	Leu	Tyr	Ala	Arg
			100					105					110		
Tyr	Arg	Val	Ile	His	Phe	Ile	Ala	Val	Ala	Val	Cys	Leu	Leu	Gly	Val
		115					120					125			
Gly	Thr	Met	Val	Gly	Ala	Asp	Ile	Leu	Ala	Gly	Arg	Glu	Asp	Asn	Ser
	130					135					140				
Gly	Ser	Asp	Val	Leu	Ile	Gly	Asp	Val	Leu	Val	Leu	Leu	Gly	Ala	Ser
145					150					155					160
Leu	Tyr	Ala	Val	Ser	Asn	Val	Cys	Glu	Glu	Tyr	Ile	Val	Lys	Lys	Leu
				165					170					175	
Ser	Arg	Gln	Glu	Phe	Leu	Gly	Met	Val	Gly	Leu	Phe	Gly	Thr	Ile	Ile
			180					185					190		
Ser	Gly	Ile	Gln	Leu	Leu	Ile	Val	Glu	Tyr	Lys	Asp	Ile	Ala	Ser	Ile
		195					200					205			
His	Trp	Asp	Trp	Lys	Ile	Ala	Leu	Leu	Phe	Val	Ala	Phe	Ala	Leu	Cys
	210					215					220				
Met	Phe	Cys	Leu	Tyr	Ser	Phe	Met	Pro	Leu	Val	Ile	Lys	Val	Thr	Ser
225					230					235					240
Ala	Thr	Ser	Val	Asn	Leu	Gly	Ile	Leu	Thr	Ala	Asp	Leu	Tyr	Ser	Leu
				245					250					255	
Phe	Phe	Gly	Leu	Phe	Leu	Phe	Gly	Tyr	Lys	Phe	Ser	Gly	Leu	Tyr	Ile
			260					265					270		
Leu	Ser	Phe	Ala	Val	Ile	Met	Val	Gly	Phe	Ile	Leu	Tyr	Cys	Ser	Thr
		275					280					285			
Pro	Thr	Arg	Thr	Ala	Glu	Pro	Ala	Glu	Ser	Ser	Val	Pro	Pro	Pro	Val
	290					295					300				
Thr	Ser	Ile	Gly	Ile	Asp	Asn	Leu	Gly	Leu	Lys	Leu	Glu	Glu	Asn	Leu
305					310					315					320
Pro	Glu	Thr	His	Ser	Val	Ala	Leu								
				325											

<210> 54
<211> 407
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Clone 5E7 from BMEC from swine brain

<400> 54
acagactgag atttagatgt ttcattggcc gtctgaagag gtgtggcttg tcttttatat 60
agagatctac attataaaat actccgtgaa gaaaaacaca ccaaacgaaa gagattttaa 120
gaatttggca cagttagtcc ctttgtgtaa tctgaactct tctagctgct gaatatcttg 180
aagtcattcc tgttcactga agtctttctg attgagctgg ttgaatactt tgaaaaatga 240
tgcgttctag ctgttgaaat ggatttccca ataggggttc ctgcatatta cctgtatagt 300
agctctatgc atatgtttct gtgcatgctc tctacccagt tgtaaggtgt cactgtattt 360
taactgttgc acttgtcaac tttcaataaa gcatataaaa tgttggt 407

<210> 55
<211> 1905
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: cDNA of
TSC-22 from BMEC from swine brain

<220>
<221> CDS
<222> (243)..(677)

<400> 55
agtctagagc ctagtggagc ccggctgccg acctgggagc cttctccgca cagcagttgg 60

atctgcatct tcccggaatc gccaagcccc agaagccggg tttctttcaa ttagggttgc 120

tgttttctgt tcctccctga gccgcataaa gctagaagat ttttatctag ctcaaacaag 180

gcctctagaa ttccctcttt tttaattttt ttcctgcgag ggtgtttttt ggctgcaatt 240

gc atg aaa tcc caa tgg tgt aga cca gtg gcg atg gat cta gga gtt 287
Met Lys Ser Gln Trp Cys Arg Pro Val Ala Met Asp Leu Gly Val
1 5 10 15

tac caa ctg aga cat ttt tca att tct ttc ttg tca tcc ttg ctc ggg 335
Tyr Gln Leu Arg His Phe Ser Ile Ser Phe Leu Ser Ser Leu Leu Gly
20 25 30

act gaa aac gcc tct gtg aga ctt gac aat agc tct tct ggt gca agt 383
Thr Glu Asn Ala Ser Val Arg Leu Asp Asn Ser Ser Ser Gly Ala Ser
35 40 45

gtg gta gct att gac aac aaa atc gag caa gct atg gat ctg gtg aaa 431
Val Val Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys
50 55 60

agc cat ttg atg tat gca gtt aga gag gaa gtg gag gtc ctc aaa gag 479
Ser His Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu
65 70 75

caa atc aaa gaa cta ata gag aaa aat tcc cag ctg gag cag gaa aac 527
Gln Ile Lys Glu Leu Ile Glu Lys Asn Ser Gln Leu Glu Gln Glu Asn
80 85 90 95

aat ctg ctg aag aca ctg gcc agt ccg gag cag ctt gcc cag ttc cag 575
Asn Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Ala Gln Phe Gln
100 105 110

gcc cag ctg cag act ggc tcc ccg ccg gcc acc aca cag ccc cag ggg 623
Ala Gln Leu Gln Thr Gly Ser Pro Pro Ala Thr Thr Gln Pro Gln Gly
115 120 125

acc aca cag ccc ccg gcc cag cca gcg tcc cag ggc tca gga ccg acc 671
Thr Thr Gln Pro Pro Ala Gln Pro Ala Ser Gln Gly Ser Gly Pro Thr
130 135 140

gcg tag cctcctaggc ccccccgcag aactggctgc tgctgtctga accgactgac 727
Ala
145

cgaccgaccg accggagagg atgtgctggg ggaggggggg gtccgcctcc accacggtca 787

cccatttcaa tgctcagctg cgaaagagac gtgagactga catatgccat tatctctttt 847

ttccagtatt aaaccctcat gtgcttttgg cttgaagaag tttcttagtt gggcgactta 907

aaggttaacc agagaattag catggatgta ctgggacctc atgcagcggg gcagatccgt 967

gagaaatggt ttcattcatg ctgaggagct gtgtgccttt ccgcccctcc cctgctccgc 1027

acccccacct ccacccccac ccctacccct acccccacct ccgagaggtc gtcgtgcttg 1087

ctcctggcgt gctgcgcgca gtccccaagc cgtggagcgc cactggactc tcctctcgct 1147

cctcccccac gaggaaccgg aaaggggggt gaaagtcaag accgaagctt catctcacct 1207

cggaggaggg gaaacgtagg tcattgtaca cgttgacgac tgtcaccaaa atccataaaa 1267

aaacgaaaca aaaacccaag agtactgtgc ctcttcccaa agcaagggat gacgcgggac 1327

tattccagag tgactgaagg gtgacaggta gctggcacct cggctatcaa cgtgaaggyg 1387

gttttgctca ttgtatattt gtgtatgtag gtgtaactat tttgtacaat agaggactgt 1447

aactactatt tagcttgtac agactgagat ttagatgttt cattggccgt ctgaagargt 1507

gtggcttgtc ttttatatag agatctacat tataaaatac tccgtgaaga aaaacacacc 1567

aaacgaaaga gattttaaga atttggcaca gttagtccct ttgtgtaatc tgaactcttc 1627

tagctgctga atatcttgaa gtcasttcct gttcactgaa gtctttctga ttgagctggt 1687

tgaatacttt gaaaaatgat gcgttctagc tgttgaaatg gatttcccaa taggggttcc 1747

tgcatattac ctgtatagta gctctatgca tatgtttctg tgcatgctct ctacccagtt 1807

gtaaggtgtc actgtatttt aactgttgca cttgtcaact ttcaataaag catataaaat 1867

gttggtvmaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1905

<210> 56
<211> 144
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: cDNA of
TSC-22 from BMEC from swine brain

<400> 56
Met Lys Ser Gln Trp Cys Arg Pro Val Ala Met Asp Leu Gly Val Tyr
1 5 10 15
Gln Leu Arg His Phe Ser Ile Ser Phe Leu Ser Ser Leu Leu Gly Thr
20 25 30
Glu Asn Ala Ser Val Arg Leu Asp Asn Ser Ser Ser Gly Ala Ser Val
35 40 45
Val Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Ser
50 55 60
His Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln
65 70 75 80
Ile Lys Glu Leu Ile Glu Lys Asn Ser Gln Leu Glu Gln Glu Asn Asn
85 90 95
Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Ala Gln Phe Gln Ala
100 105 110

Gln Leu Gln Thr Gly Ser Pro Pro Ala Thr Thr Gln Pro Gln Gly Thr
115 120 125
Thr Gln Pro Pro Ala Gln Pro Ala Ser Gln Gly Ser Gly Pro Thr Ala
130 135 140

<210> 57
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 57
aagaggtgtg gcttgtcttt ta 22

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 58
tttttcaaag tattcaacca gctc 24